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⌐ 1: P54967 **BIOTIN SYNTHASE**   BLink, PubMed, Related Sequences, Taxonomy, LinkOut
**(BIOTIN
SYNTHETASE)**

```
LOCUS       BIOB_ARATH      378 aa                    PLN        01-OCT-2000
DEFINITION  BIOTIN SYNTHASE (BIOTIN SYNTHETASE).
ACCESSION   P54967
PID         g1705463
VERSION     P54967  GI:1705463
DBSOURCE    swissprot: locus BIOB_ARATH, accession P54967;
            class: standard.
            created: Oct 1, 1996.
            sequence updated: Oct 1, 1996.
            annotation updated: Oct 1, 2000.
            xrefs: gi: gi: 1045315, gi: gi: 1045316, gi: gi: 1403661, gi: gi:
            1403662, gi: gi: 1769456, gi: gi: 1769457, gi: gi: 6598343, gi: gi:
            2288983
            xrefs (non-sequence databases): InterPro IPR002684, Pfam PF01792
KEYWORDS    Biotin biosynthesis; Iron-sulfur; Transferase.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
            Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (residues 1 to 378)
  AUTHORS   Weaver,L.M., Yu,F., Wurtele,E.S. and Nikolau,B.J.
  TITLE     Characterization of the cDNA and gene coding for the biotin
            synthase of Arabidopsis thaliana
  JOURNAL   Plant Physiol. 110 (3), 1021-1028 (1996)
  MEDLINE   96417082
  REMARK    SEQUENCE FROM N.A.
            STRAIN=CV. LANDSBERG ERECTA
REFERENCE   2  (residues 1 to 378)
  AUTHORS   Patton,D., Pacella,M. and Ward,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (??-JUL-1996)
  REMARK    SEQUENCE FROM N.A.
            STRAIN=CV. COLUMBIA; TISSUE=Leaf
REFERENCE   3  (residues 1 to 378)
  AUTHORS   Baldet,P. and Ruffet,M.L.
  TITLE     Biotin synthesis in higher plants: isolation of a cDNA encoding
            Arabidopsis thaliana bioB-gene product equivalent by functional
            complementation of a biotin auxotroph mutant bioB105 of Escherichia
            coli K12
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 319 (2), 99-106 (1996)
  MEDLINE   96307524
  REMARK    SEQUENCE FROM N.A.
            STRAIN=CV. COLUMBIA; TISSUE=Leaf
REFERENCE   4  (residues 1 to 378)
  AUTHORS   Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D.,
            Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E.,
            Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M.,
            Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L.,
            Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,
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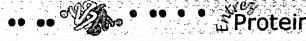
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                        Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
                        Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
                        Venter,J.C.
        TITLE           Sequence and analysis of chromosome 2 of the plant Arabidopsis
                        thaliana
        JOURNAL         Nature 402 (6763), 761-768 (1999)
        MEDLINE         20083487
        REMARK          SEQUENCE FROM N.A.
                        STRAIN=CV. COLUMBIA
    COMMENT             ------------------------------------------------------------
                        This SWISS-PROT entry is copyright. It is produced through a
                        collaboration between the Swiss Institute of Bioinformatics and
                        the EMBL outstation - the European Bioinformatics Institute.
                        The original entry is available from http://www.expasy.ch/sprot
                        and http://www.ebi.ac.uk/sprot
                        ------------------------------------------------------------.
                        [CATALYTIC ACTIVITY] DETHIOBIOTIN + (S) = BIOTIN.
                        [PATHWAY] LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
                        [SIMILARITY] BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
                        FAMILY.
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                        /db_xref="taxon:3702"
                        1..378
        Protein         1..378
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                        /EC_number="2.8.1.6"
        Site            94
                        /site_type="metal-binding"
                        /note="IRON-SULFUR (POTENTIAL)."
        Site            98
                        /site_type="metal-binding"
                        /note="IRON-SULFUR (POTENTIAL)."
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                        /site_type="metal-binding"
                        /note="IRON-SULFUR (POTENTIAL)."
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           61 lldllfhgaq vhrhvhnfre vqqctllsik tggcsedcsy cpqssrystg vkaqrlmskd
          121 avidaakkak eagstrfcmg aawrdtigrk tnfsqileyi keirgmgmev cctlgmiekq
          181 qalelkkagl taynhnldts reyypnvitt rsyddrletl shvrdaginv csggiiglge
          241 aeedrigllh tlatlpshpe svpinallav kgtpledqkp veiwemirmi gtarivmpka
          301 mvrlsagrvr fsmseqalcf lagansiftg ekllttpnnd fdadqlmfkt lglipkppsf
          361 seddsesenc ekvasash
    //
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◻ 1: <u>CAA18303</u> **biotin synthase (EC 2.8.1.6) [Schizosaccharomyces pombe]**

BLink, Related Sequences, Nucleotide, Taxonomy

```
LOCUS       CAA18303         363 aa                    PLN        06-APR-1999
DEFINITION  biotin synthase (EC 2.8.1.6) [Schizosaccharomyces pombe].
ACCESSION   CAA18303
PID         g2995363
VERSION     CAA18303.1  GI:2995363
DBSOURCE    embl locus SPCC320, accession AL022245.2
KEYWORDS    .
SOURCE      fission yeast.
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 363)
  AUTHORS   Wood,V., Rajandream,M.A., Barrell,B.G., Wedler,H., Wambutt,R. and
            Wedler,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-1998) European Schizosaccharomyces genome
            sequencing project, Sanger Centre, The Wellcome Trust Genome
            Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk
            and AGOWA GmbH, Glienicker Weg 185, D-12489 Berlin, Germany
COMMENT     Notes:
            Protein coding regions (CDS) have been predicted with the help of
            computer analysis using the Genefinder program in PomBase (an ACEDB
            database) with additional predictions for the branch-acceptor sites
            supplied by the program Sp3splice. CAUTION: It is possible that for
            any individual CDS we may have underestimated or overestimated the
            number of introns/exons or we may not have chosen the correct
            splice donor/acceptor sites. CDS are numbered using the following
            system eg SPBC25H2.01c. SP (S. pombe), B (chromosome 2), c25H2
            (cosmid name), .01 (first CDS), c (complementary strand).
            The more significant matches with motifs in the PROSITE database
            are also included but some of these may be fortuitous. The length
            in codons is given for each CDS.
            IMPORTANT: This sequence MAY NOT be the entire insert of the
            sequenced clone.  It may be shorter because we only sequence
            overlapping sections once, or longer, because we arrange for a
            small overlap between neighbouring submissions. Details of yeast
            sequencing at the Sanger Centre are available on the World Wide
            Web.
            (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
            During 1995 to 1996 about 66% of S. pombe chromosome 1 was
            sequenced by the Sanger Centre.  The sequencing of the S. pombe
            genome is now being continued with funding from The European
            Commission. Fourteen European sequencing laboratories, including
            the Sanger Centre, are participating in the project.
            Cosmid c320 is overlapped by cosmid c330 at the 5' end and c1235 at
            the 3' end.
FEATURES             Location/Qualifiers
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                     /organism="Schizosaccharomyces pombe"
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                       /db_xref="taxon:4896"
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                       /map="IIIL"
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        Protein        1..363
                       /product="biotin synthase (EC 2.8.1.6)"
        CDS            1..363
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                       /label=bio2
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                       /coded_by="AL022245.2:38444..39535"
                       /note="SPCC320.01c, len:362"
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         61 llsiktggct edckycaqss ryntgvkatk lmkidevlek akiakakgst rfcmgsawrd
        121 lngrnrtfkn ileiikevrs mdmevcvtlg mlneqqakel kdagltaynh nldtsreyys
        181 kiistrtyde rlntidnlrk aglkvcsggi lglgekkhdr vglihslatm pthpesvpfn
        241 llvpipgtpv gdavkerlpi hpflrsiata ricmpktiir faagrntcse seqalafmag
        301 anavftgekm lttpavswds dsqlfynwgl egmqsfeygt stegedgtft lppkerlaps
        361 psl
//
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▢ 1: NP_011802 **Biotin synthase; BLink, PubMed, Related Sequences, Nucleotide, Genome, T**
Bio2p
[Saccharomyces
cerevisiae]

```
LOCUS       NP_011802       375 aa                    PLN       30-JAN-2001
DEFINITION  Biotin synthase; Bio2p [Saccharomyces cerevisiae].
ACCESSION   NP_011802
PID         g6321725
VERSION     NP_011802.1  GI:6321725
DBSOURCE    REFSEQ: accession NC_001139.1
KEYWORDS    .
SOURCE      baker's yeast.
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
            Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (residues 1 to 375)
  AUTHORS   Goffeau,A., Barrell,B.G., Bussey,H., Davis,R.W., Dujon,B.,
            Feldmann,H., Galibert,F., Hoheisel,J.D., Jacq,C., Johnston,M.,
            Louis,E.J., Mewes,H.W., Murakami,Y., Philippsen,P., Tettelin,H. and
            Oliver,S.G.
  TITLE     Life with 6000 genes
  JOURNAL   Science 274 (5287), 546 (1996)
  MEDLINE   97002444
REFERENCE   2  (residues 1 to 375)
  AUTHORS   Tettelin,H., Agostoni Carbone,M.L., Albermann,K., Albers,M.,
            Arroyo,J., Backes,U., Barreiros,T., Bertani,I., Bjourson,A.J.,
            Bruckner,M., Bruschi,C.V., Carignani,G., Castagnoli,L., Cerdan,E.,
            Clemente,M.L., Coblenz,A., Coglievina,M., Coissac,E., Defoor,E.,
            Del Bino,S., Delius,H., Delneri,D., de Wergifosse,P., Dujon,B.,
            Kleine,K. et al.
  TITLE     The nucleotide sequence of Saccharomyces cerevisiae chromosome VII
  JOURNAL   Nature 387 (6632 Suppl), 81-84 (1997)
  MEDLINE   97313265
REFERENCE   3  (residues 1 to 375)
  AUTHORS   Saccharomyces Genome Database (yeast-curator@genome.stanford.edu).
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-1999) Department of Genetics, Stanford
            University, Saccharomyces Genome Database, Stanford, CA 94305-5120,
            USA
COMMENT     REFSEQ: This reference sequence was provided by the Saccharomyces
            Genome Database (SGD).
            Method: conceptual translation.
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     Protein         1..375
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                     /note="Bio2p"
     CDS             1..375
                     /gene="BIO2"
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       61 iyhtpllelt haaqlqhrkw hdptkvqlct lmniksggcs edckycaqss rndtglkaek
      121 mvkvdevike aeeakrngst rfclgaawrd mkgrksamkr iqemvtkvnd mgletcvtlg
      181 mvdqdqakql kdagltaynh nidtsrehys kvittrtydd rlqtiknvqe sgikactggi
      241 lglgeseddh igfiytlsnm sphpeslpin rlvaikgtpm aeeladpksk klqfdeilrt
      301 iatarivmpk aiirlaagry tmketeqfvc fmagcnsift gkkmlttmcn gwdedkamla
      361 kwglqpmeaf kydrs
     //
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